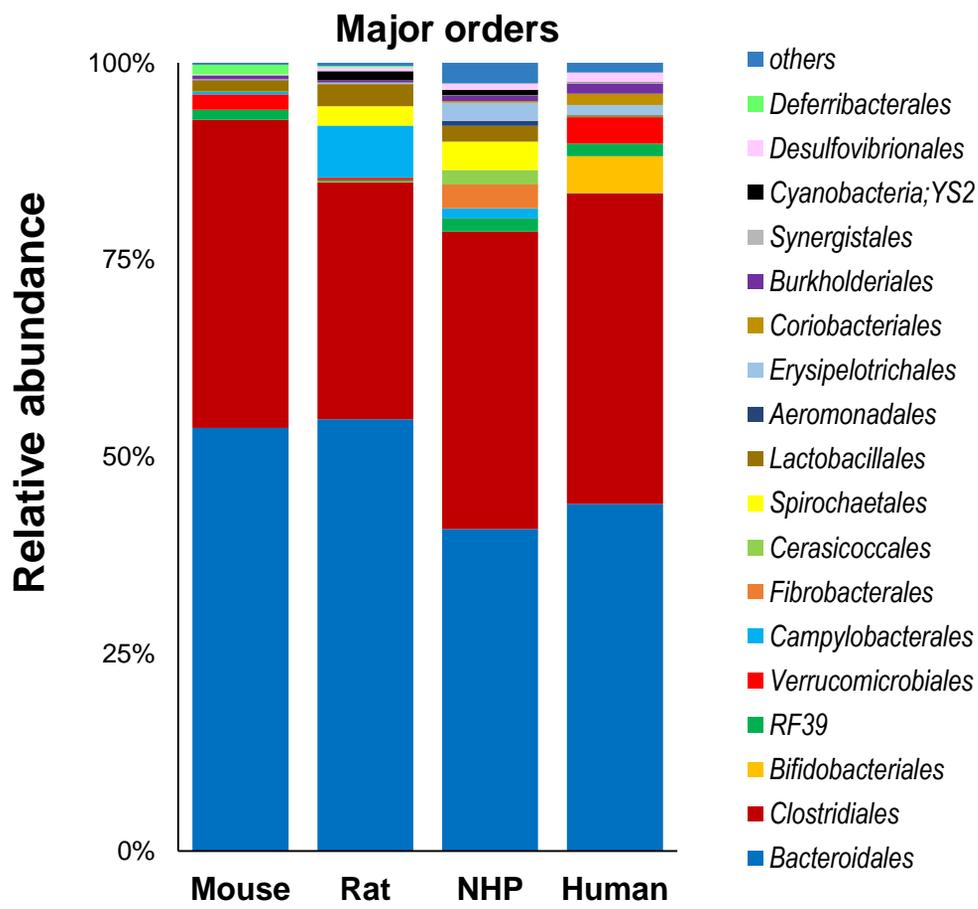
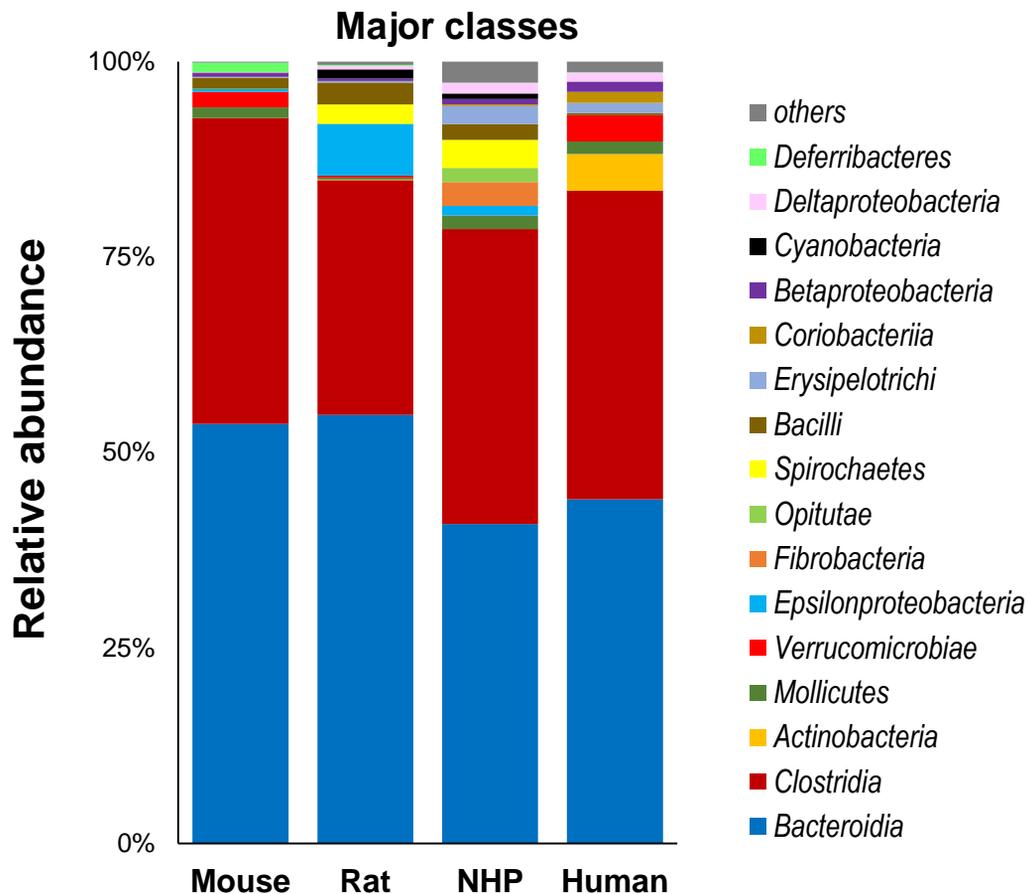
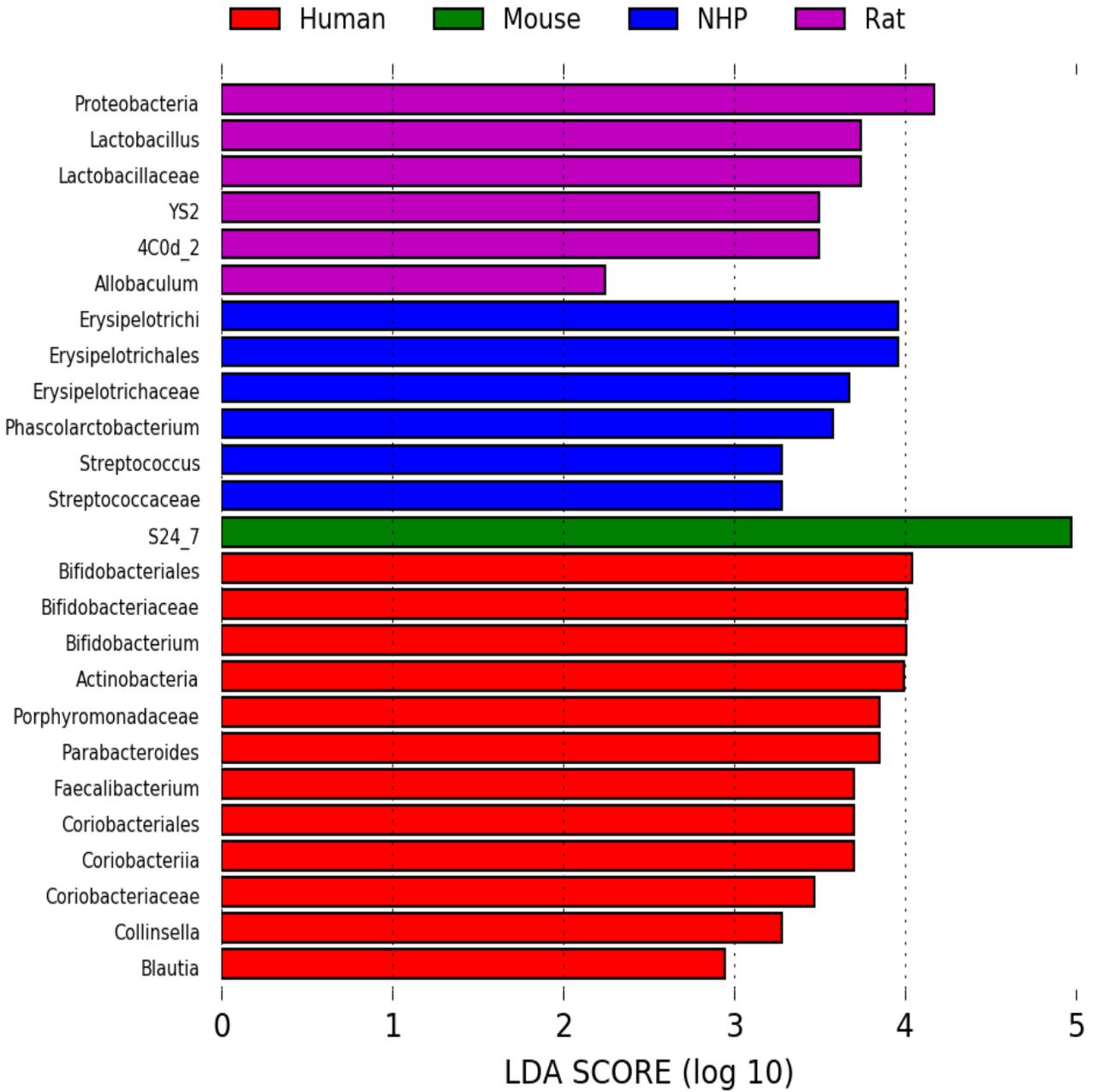


## **Supplementary material**

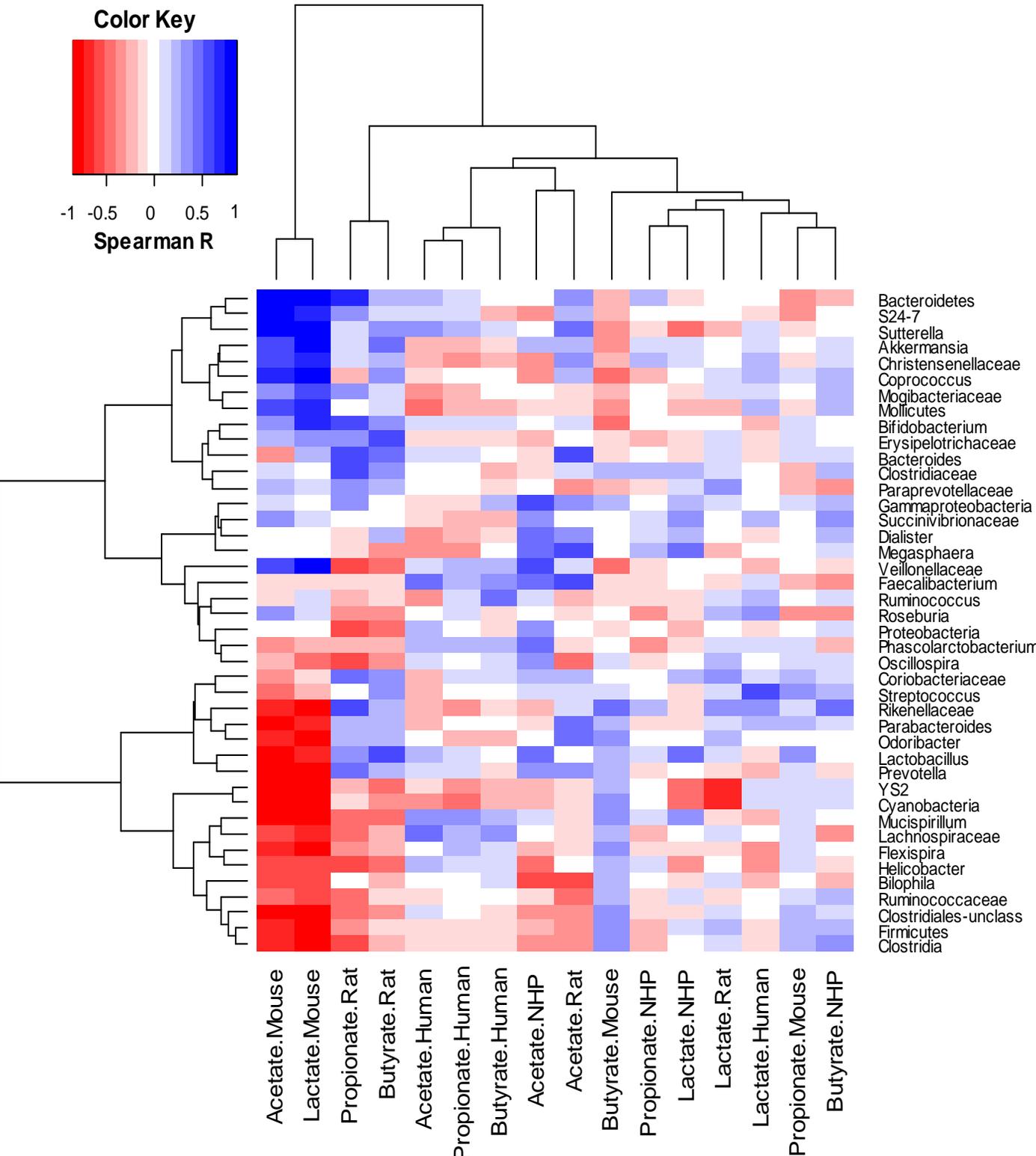
**Suppl. Fig. 1.** Mean relative abundance of major bacterial classes (a) and order (b) detected in the gut microbiome of mice, rats, non-human primates, and human subjects.



**Suppl. Fig. 2.** Linear discriminant analysis (LDA) effect size (Lefse) cladogram representing the unique bacterial signatures identified in mice, rats, non-human primates, and human subjects.



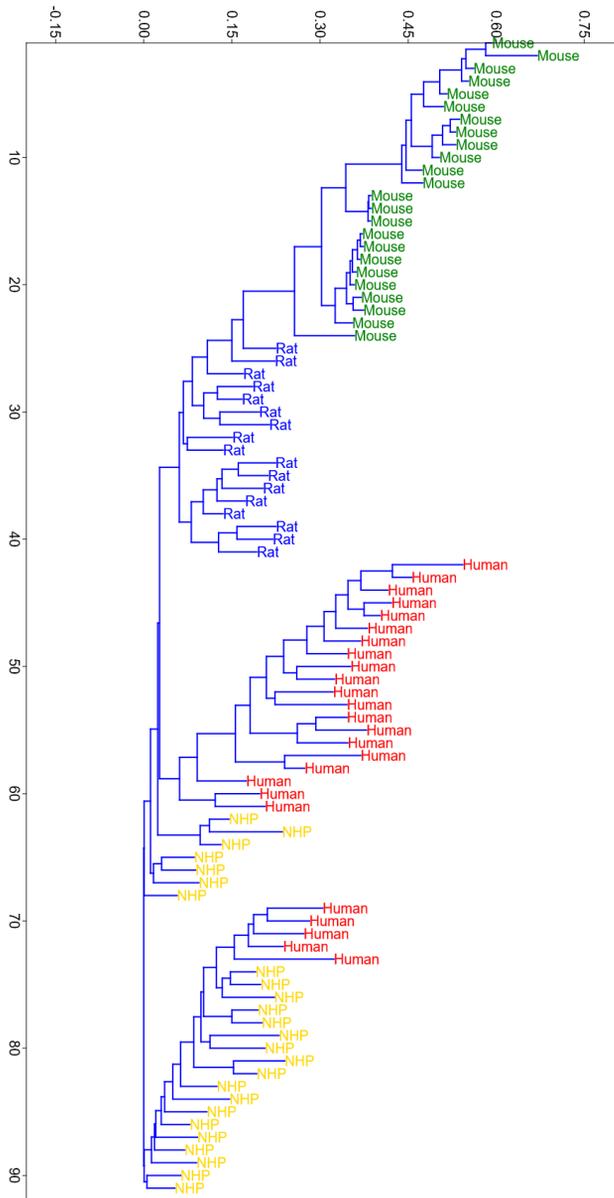
**Suppl. Fig. 3.** Heat-map representing the clustering patterns of correlation between the abundance of major gut bacterial OTUs and the fecal levels of major short-chain fatty acids in mice, rats, non-human primates, and human subjects.



**Suppl. Fig. 4.** Hierarchical clustering representing the Euclidean similarity index (a) and distance (b) between the gut microbiome of mice, rats, non-human primates, and human subjects.

**(a)**

**Neighbor Joining Clustering:  
Euclidean Similarity Index**



**(b)**

**Classical Hierarchical clustering:  
Euclidean distance**

